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Data Article

Data supporting the functional role of Eleven-nineteen Lysine-rich Leukemia 3 (ELL3) in B cell lymphoma cell line cells

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ABSTRACT

The data presented here are related to the research article entitled "Selective expression of the transcription elongation factor ELL3 in B cells prior to ELL2 drives proliferation and survival" (Alexander et al., 2017) [1]. The cited research article characterizes Eleven-nineteen Lysine-rich Leukemia 3 (ELL3) expression in the B cell compartment and functional dependence in B lymphoma cell lines. This data report describes the mRNA expression pattern in a panel of cell lines representing the B cell compartment, supplementing the protein expression data presented in the associated research report. In addition, a reanalysis is presented of publicly available mRNA expression data from primary murine B cells to reveal dynamic regulation of the ELL family members post LPS stimulation (Barwick et al., 2016) [2]. The effect of ELL3 depletion on cell morphology, latent Epstein Barr Virus (EBV) lytic replication and

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Abbreviations: ELL, Eleven-nineteen Lysine-rich Leukemia; EBV, Epstein Barr Virus; BL, Burkitt's Lymphoma
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differentiation markers in a Burkitt's lymphoma (BL) cell line cells are presented.

Specifications Table

Subject area	Immunology and Molecular Biology
More specific subject area	Transcriptional elongation
Type of data	Figures and Images
How data was acquired	– quantitative PCR (qPCR) (Bio-Rad CFX96 Real-Time PCR Detection System and CFX96 Software) – Reanalyzed publically available RNA-Seq experiment GSE70294 – Time lapse imaging (Evos Auto FL Cell Imaging System and Image Studio Software) – Western blot (SDS-Page gel electrophoresis and wet transfer; Bio-Rad equipment and Bio-Rad clarity chemiluminescent detection)
Data format	Analyzed
Experimental factors	– RNA was extracted from untransduced cell line model cells and expression assessed – RNA-Seq experiment was done on LPS treated primary murine B cells that were cell sorted by divisions and CD138 levels. – Namalwa BL cell line transduced with control and two independent mCherry-tagged ELL3 specific shRNA's for five consecutive days – Protein and mRNA was extracted from Namalwa BL cell line transduced with control and two independent mCherry-tagged ELL3 specific shRNA's for five consecutive days and expression assessed.
Experimental features	– Quantitative mRNA detection of ELL, ELL2 and ELL3 in B cell compartment cell line models – Expression levels of ELL, ELL2 and ELL3 were extracted from the data set GSE70294 of RNA-Seq performed on each Cell Titer Violet and CD138-positive, populations following LPS stimulus of murine primary B cells. – shRNA transduced Namalwa cells were imaged at day 6 post transduction every 5 min for 24 h. – Western blot analysis of PRDM1 levels and detection of PRDM1, EBV lytic replication genes (BZLF1, BMRF and BLLF1), B cell factors (BCL6, PAX5, MYC) and plasma cell factor (membrane bound and secreted IgM) mRNA levels
Data source location	H. Lee Moffitt Cancer Center and Research Institute, Tampa, FL, USA
Data accessibility	Data is within this article

Value of the data

- This data describes an expression pattern of ELL family members that is replicated in both human and murine B cell compartment
- The data shows the role of ELL3 in the morphology of B cells and reveals disruption of cell division
- The data reveals the impact of ELL3 depletion on B cell differentiation markers and latent EBV gene expression.